

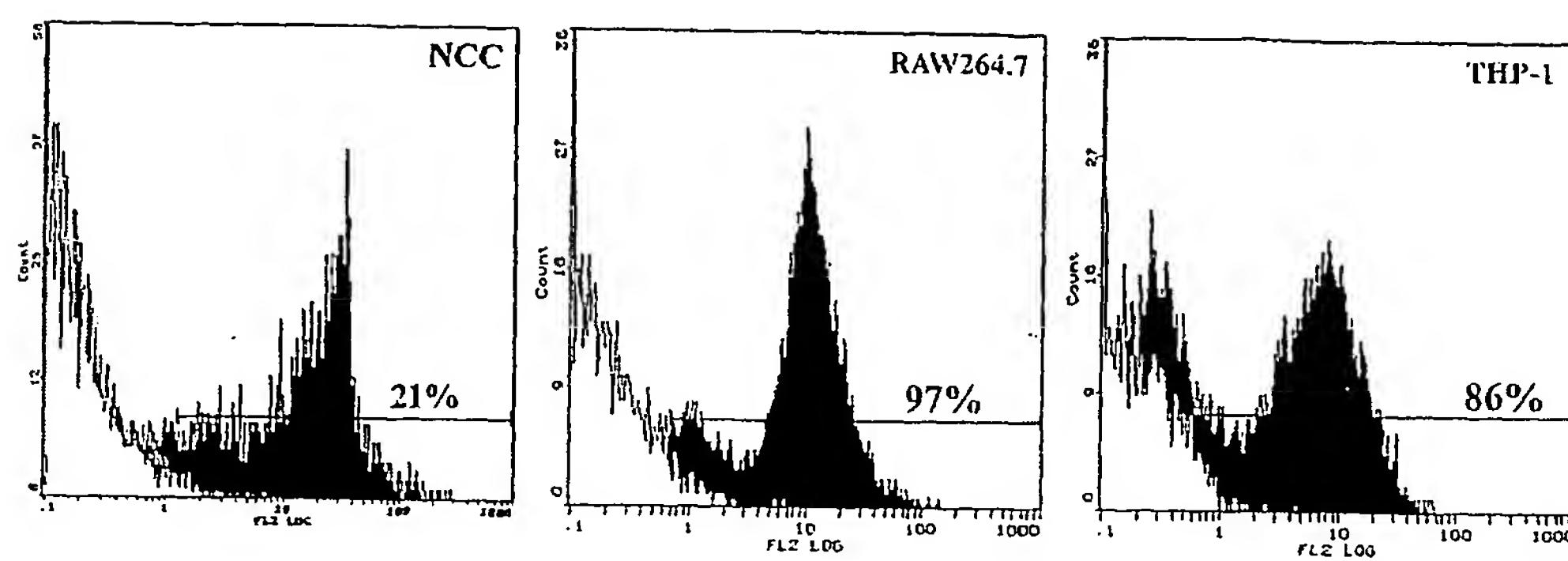
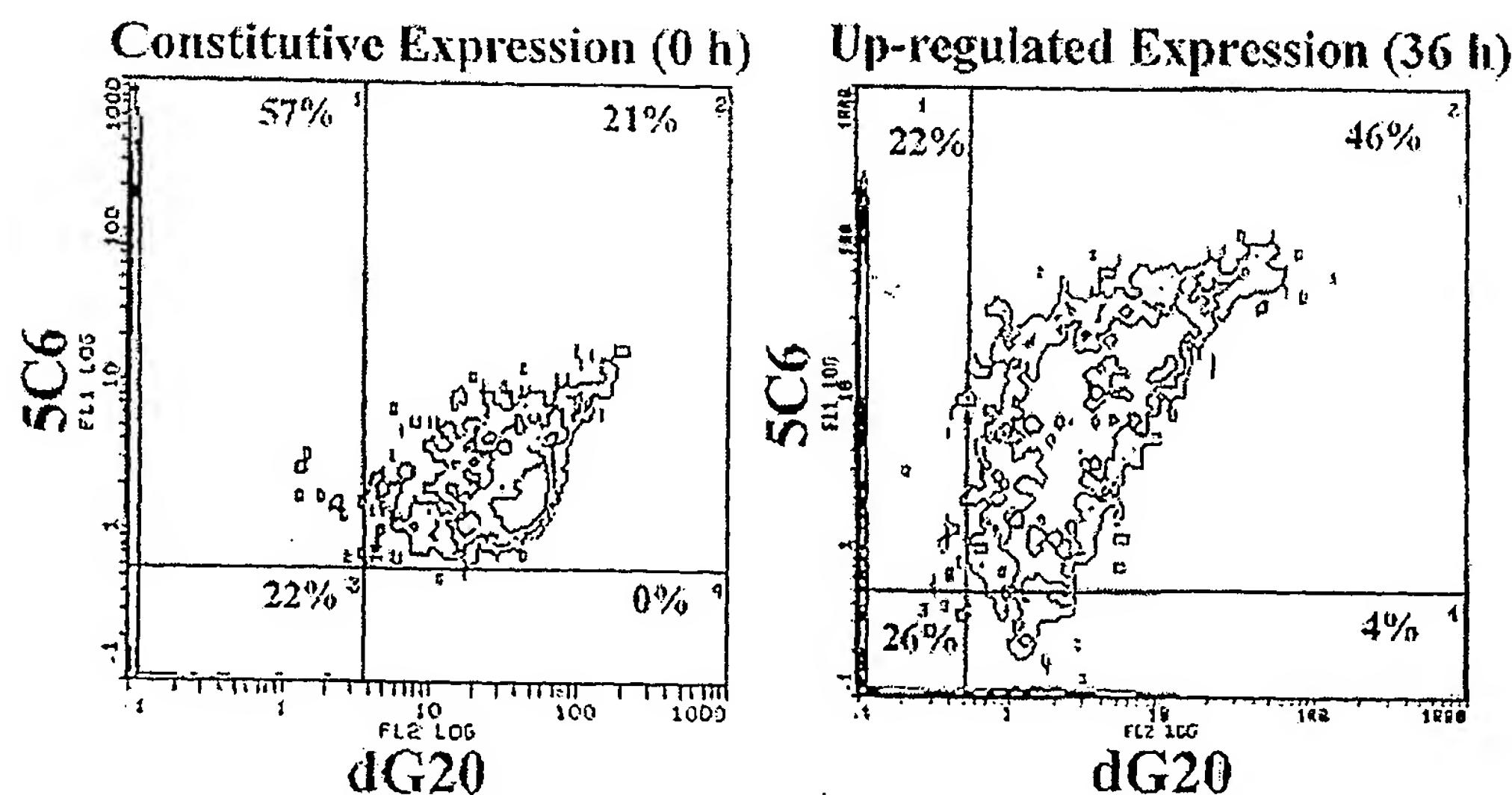
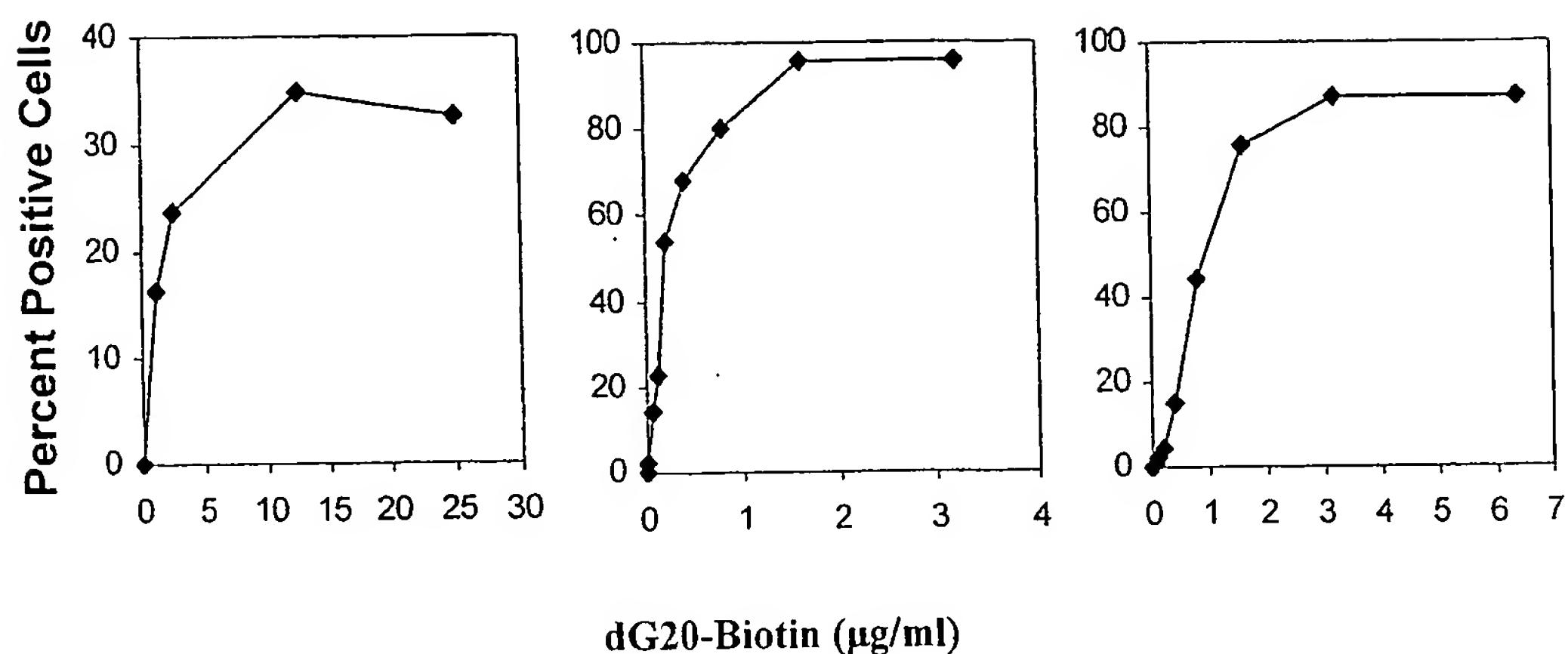
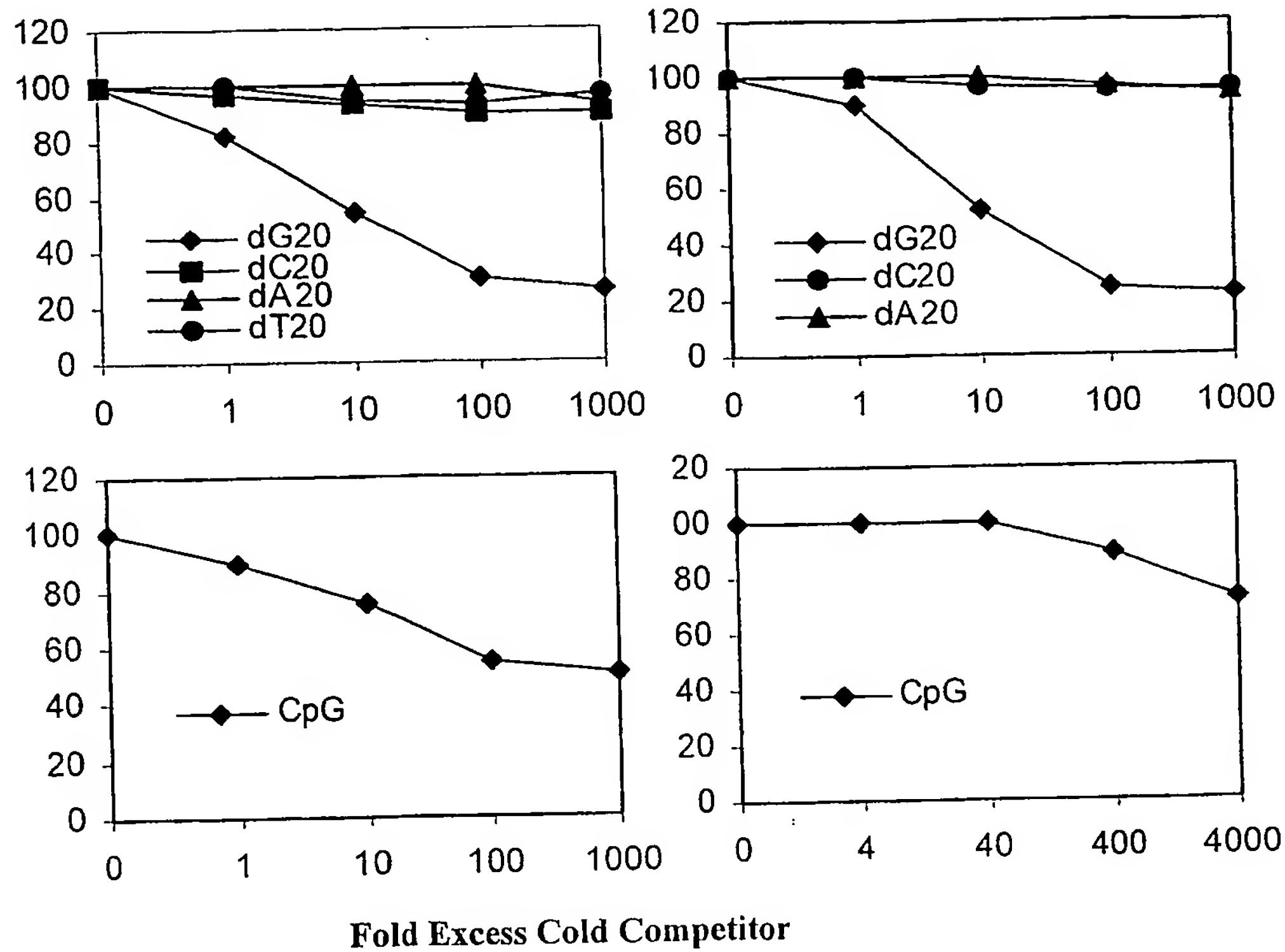
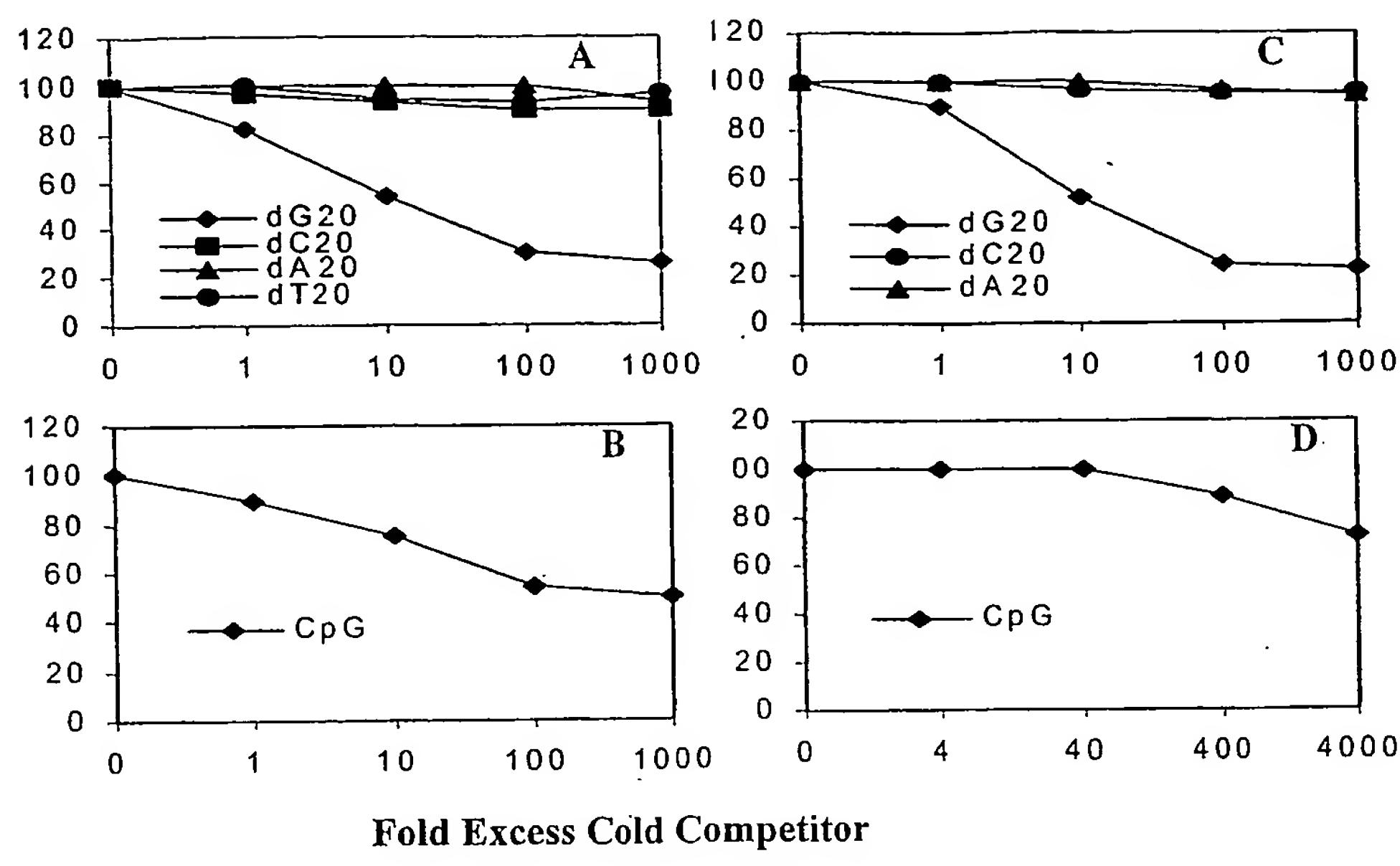
Figures 1A - 1B**A****B**

Figure 2

Figures 3A - 3D**BEST AVAILABLE COPY**

Figures 4A - 4C



A 1 2 3 4 5 6

66

45

36

29

20.1

14.2

B

kDa

66

45

36

29

20.1

14.4

C

kDa

1

2

66

45

36

29

20.1

14.4

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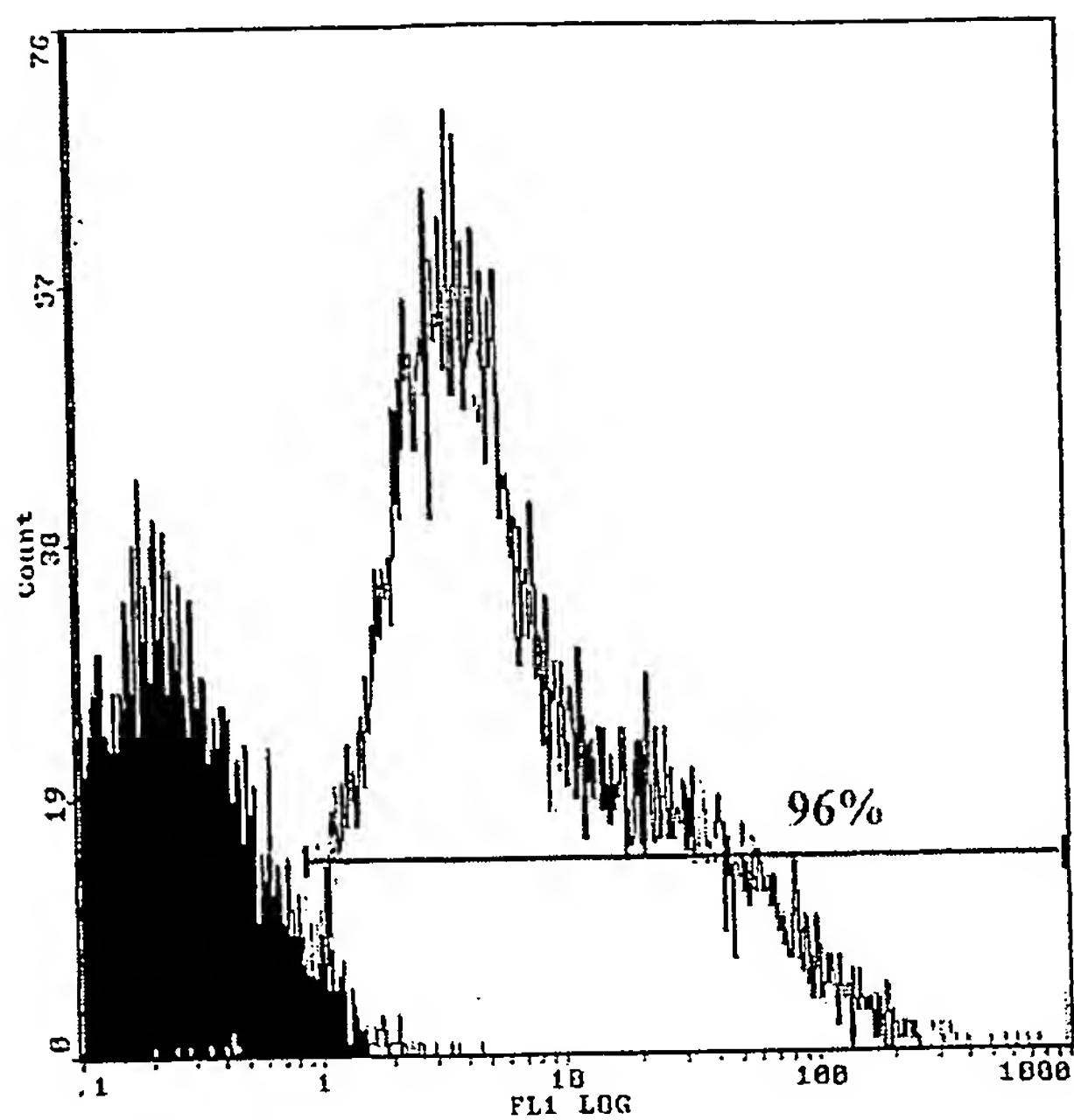
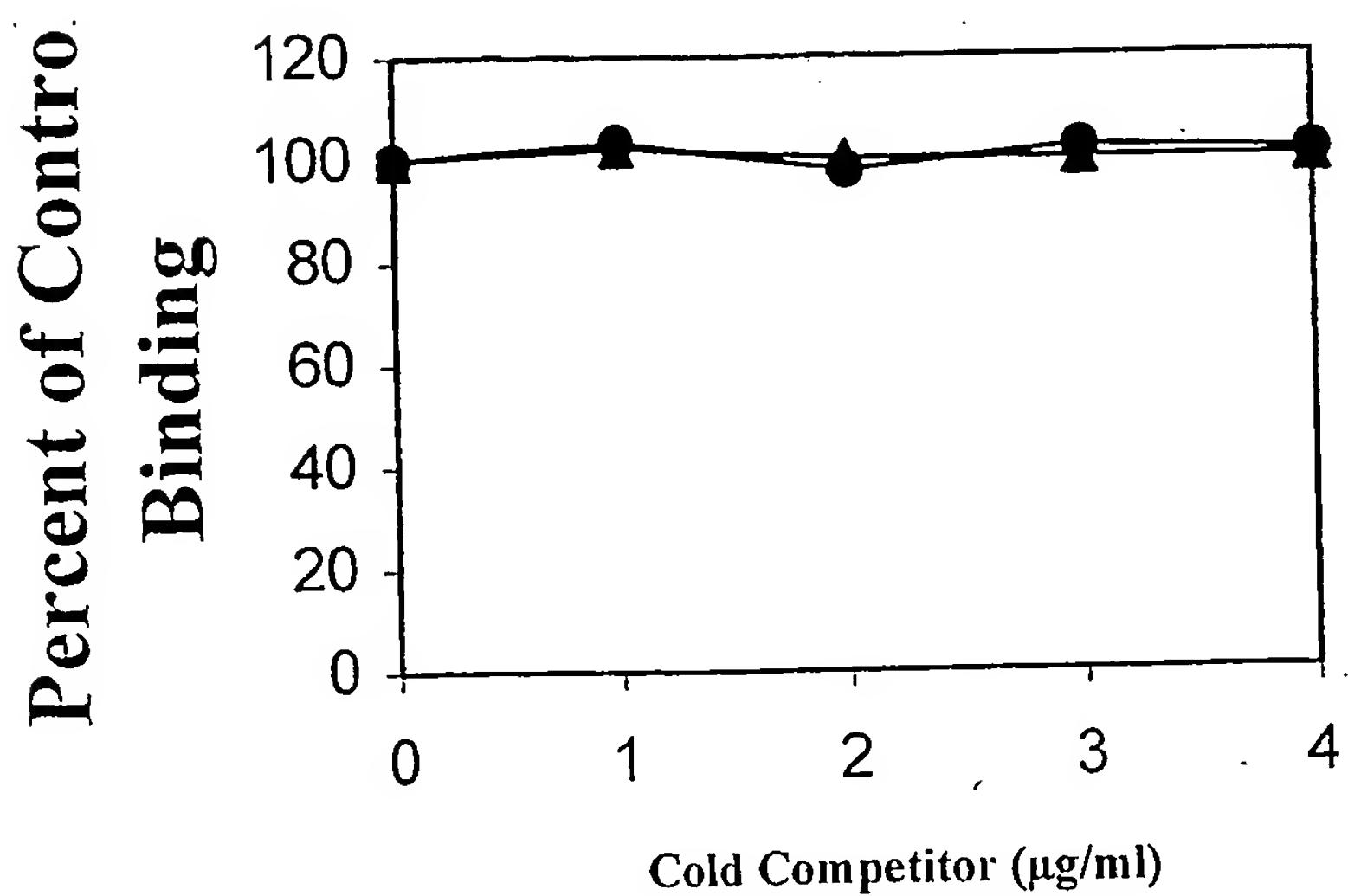
Figures 5A - 5B**A****B**

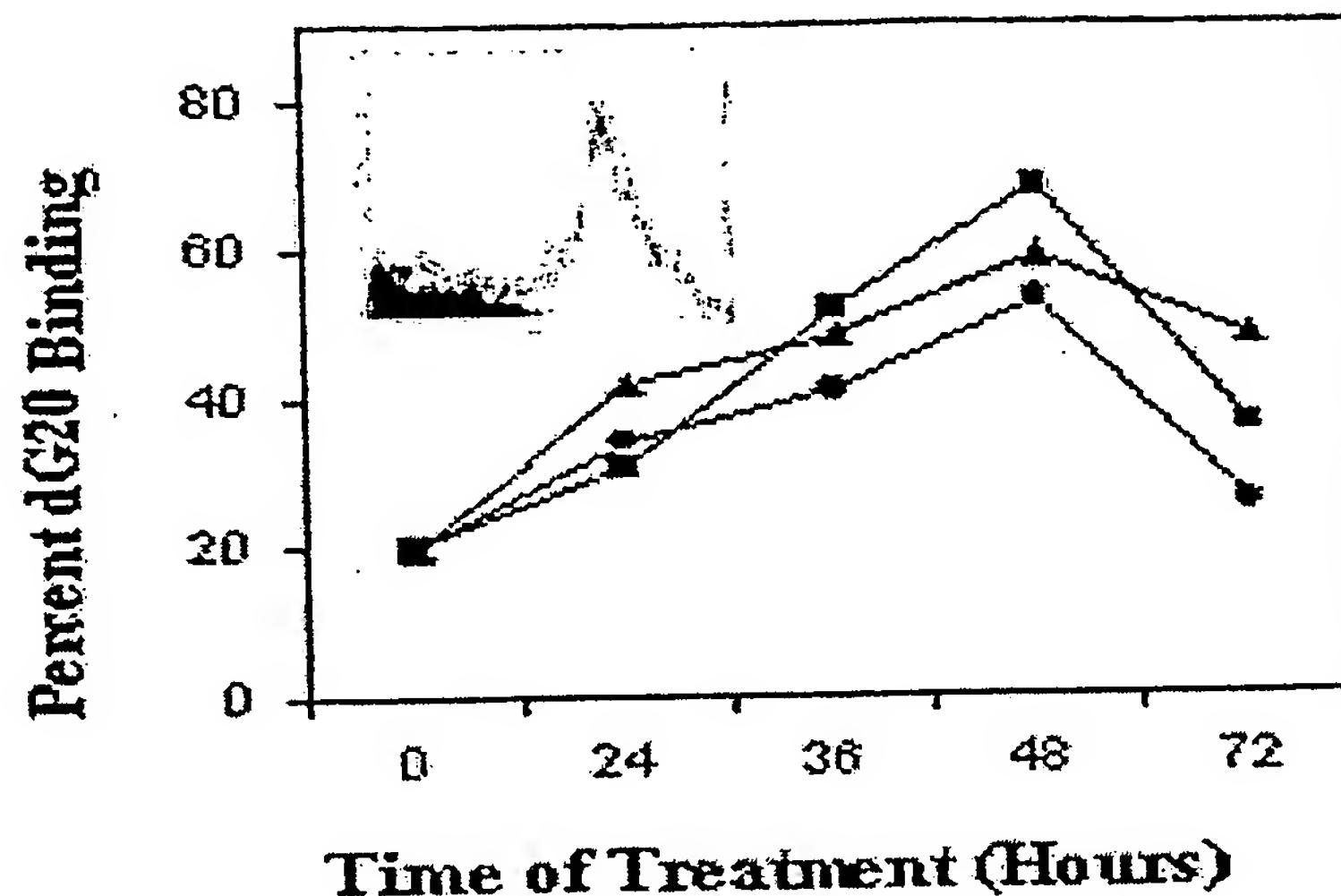
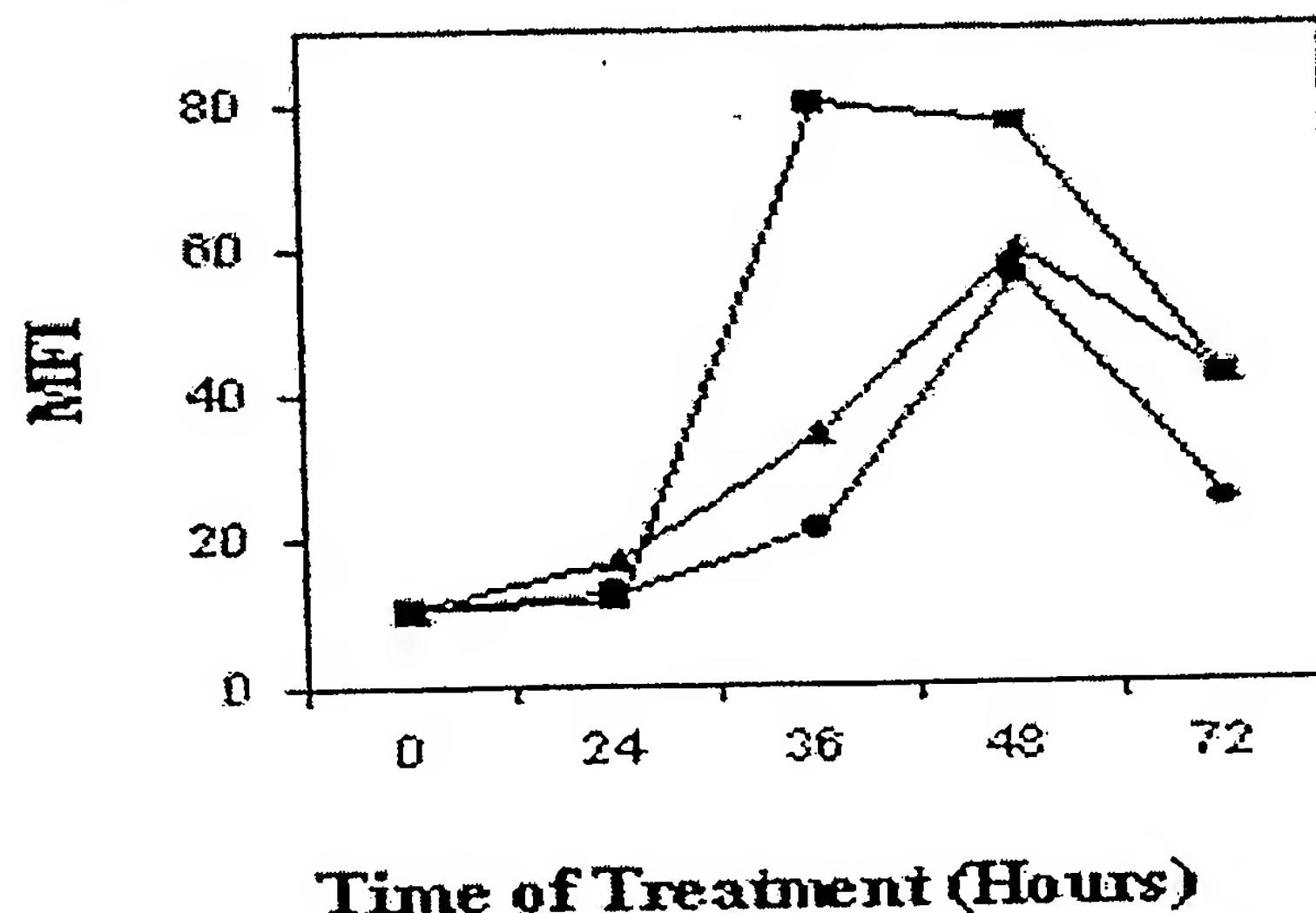
Figure 6**A****B**

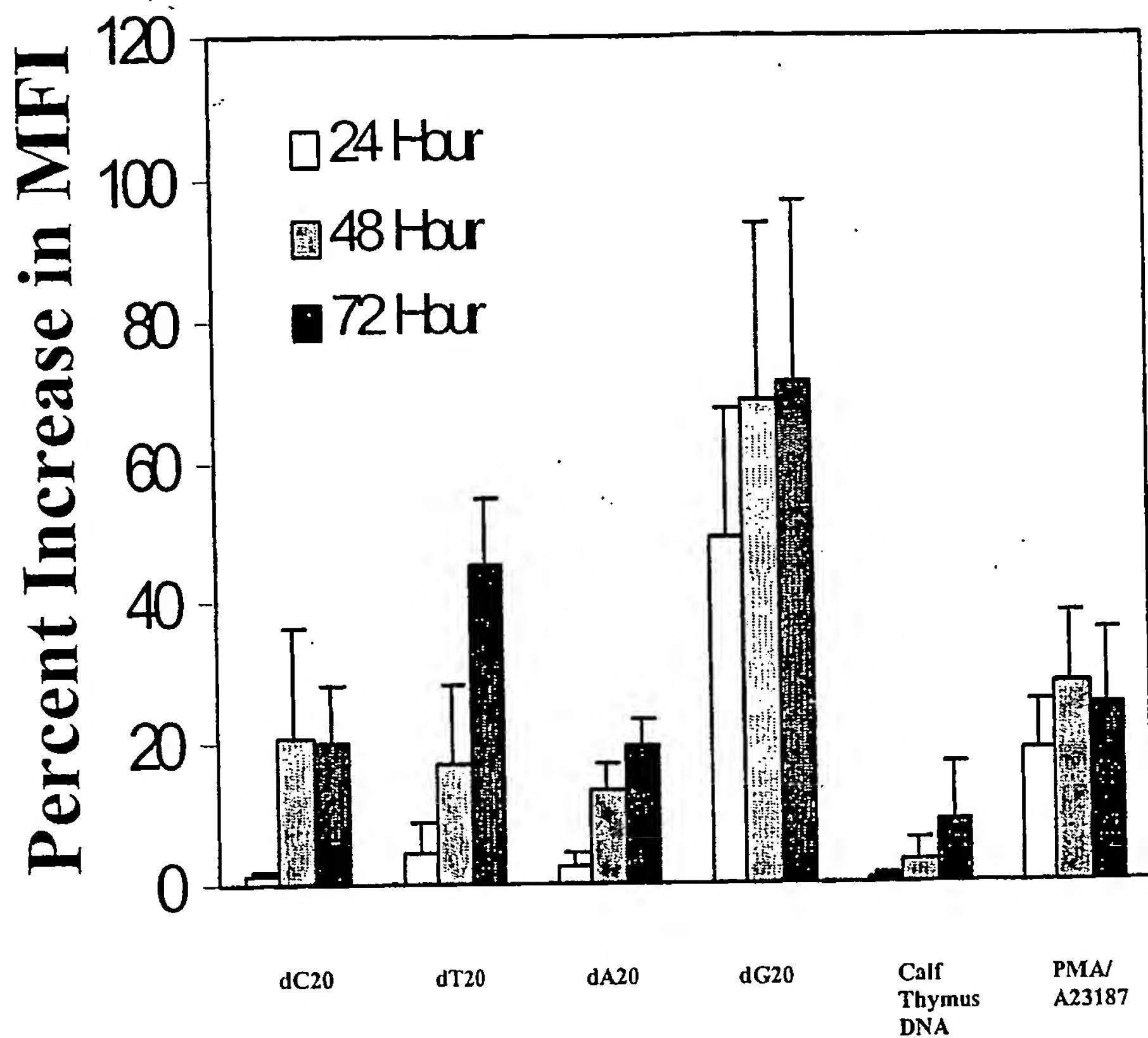
Figure 7

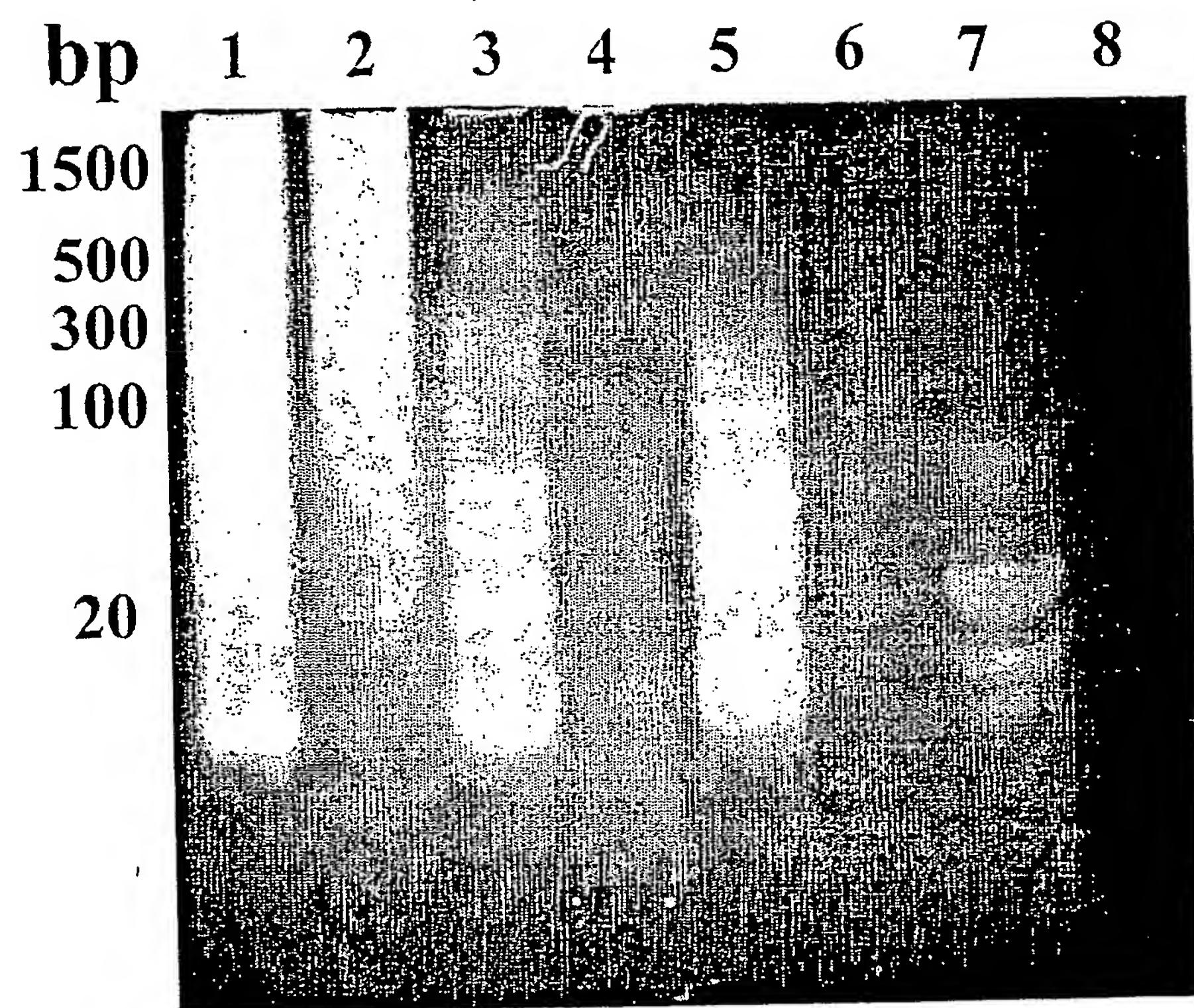
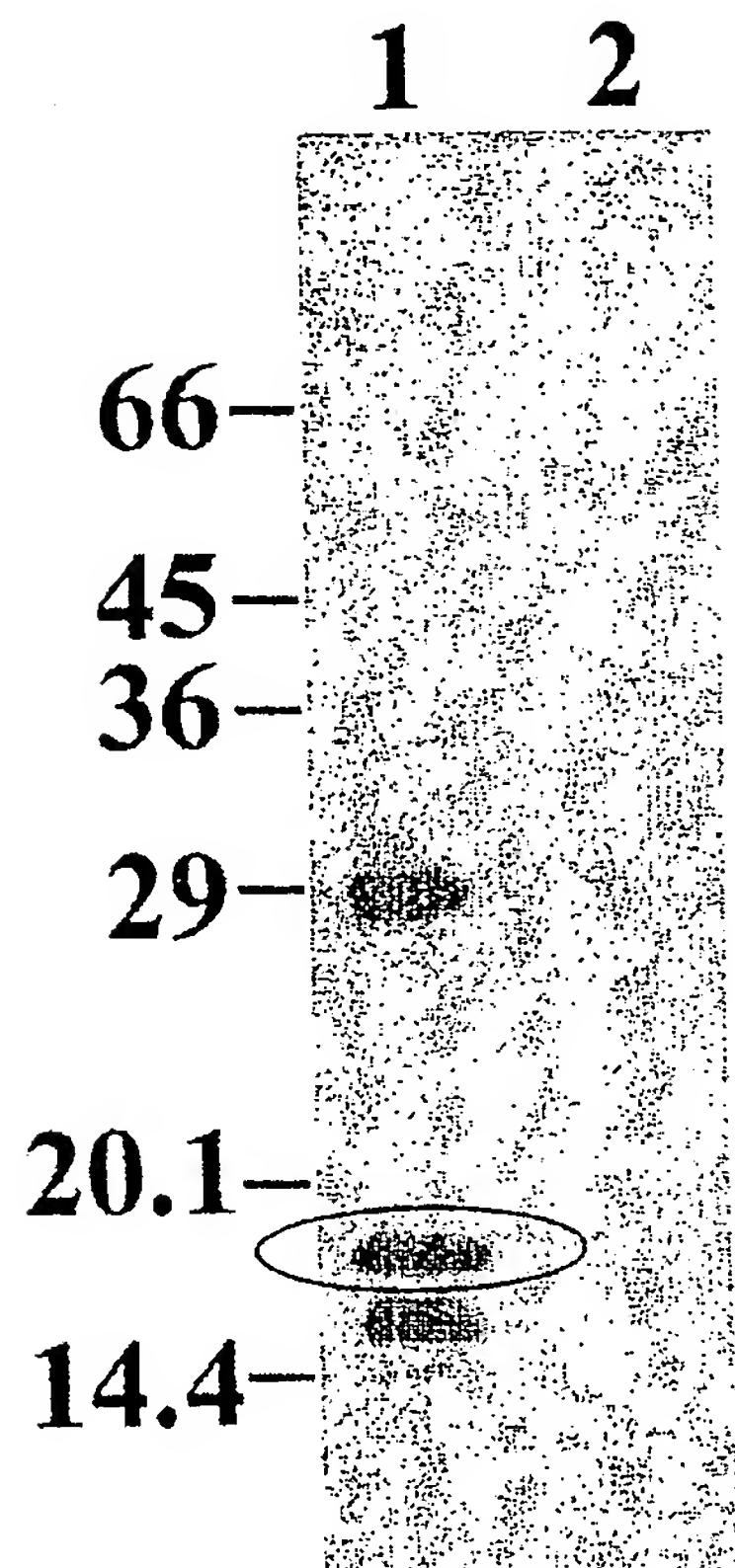
Figure 8**BEST AVAILABLE COPY**

Figure 9

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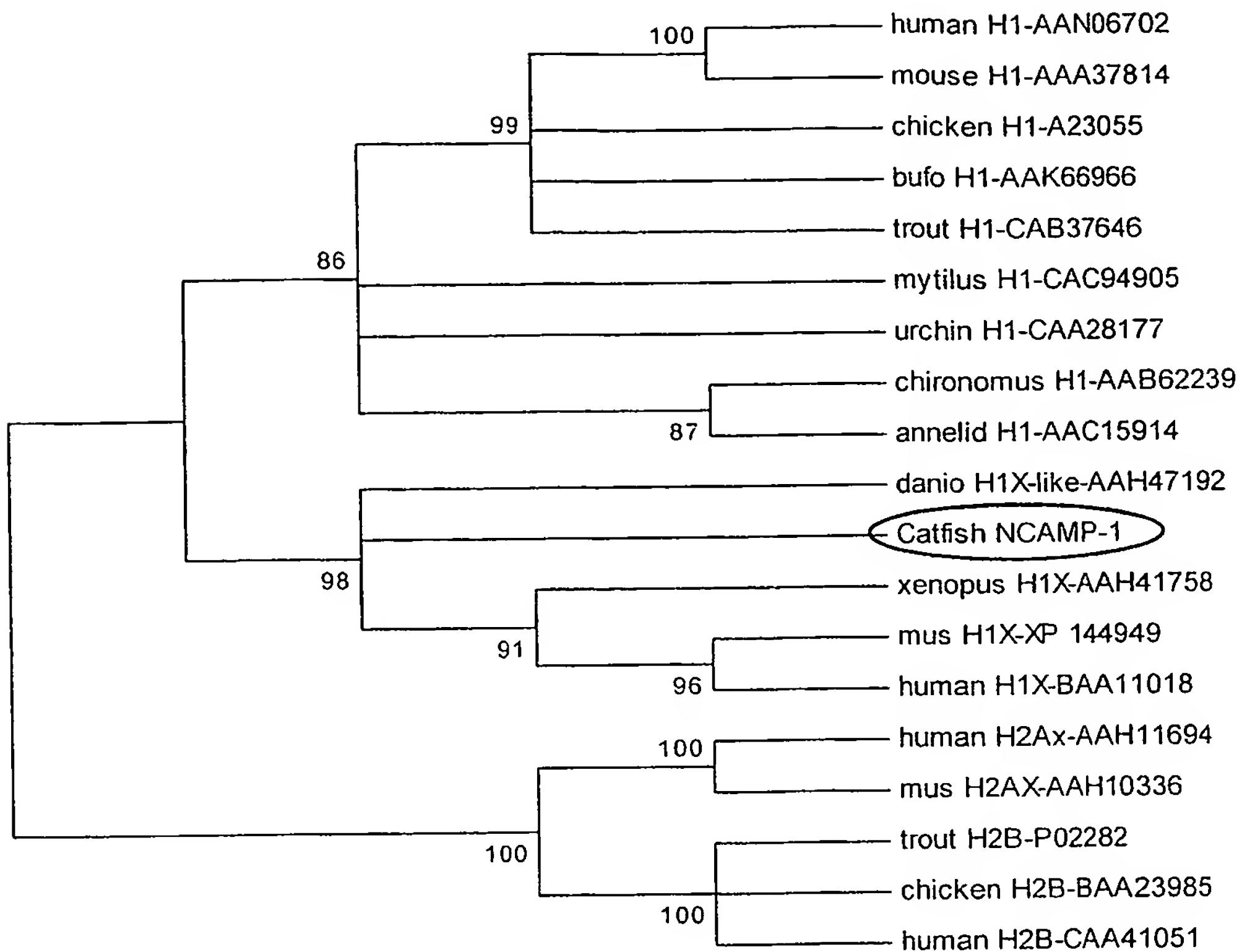
Figure 10

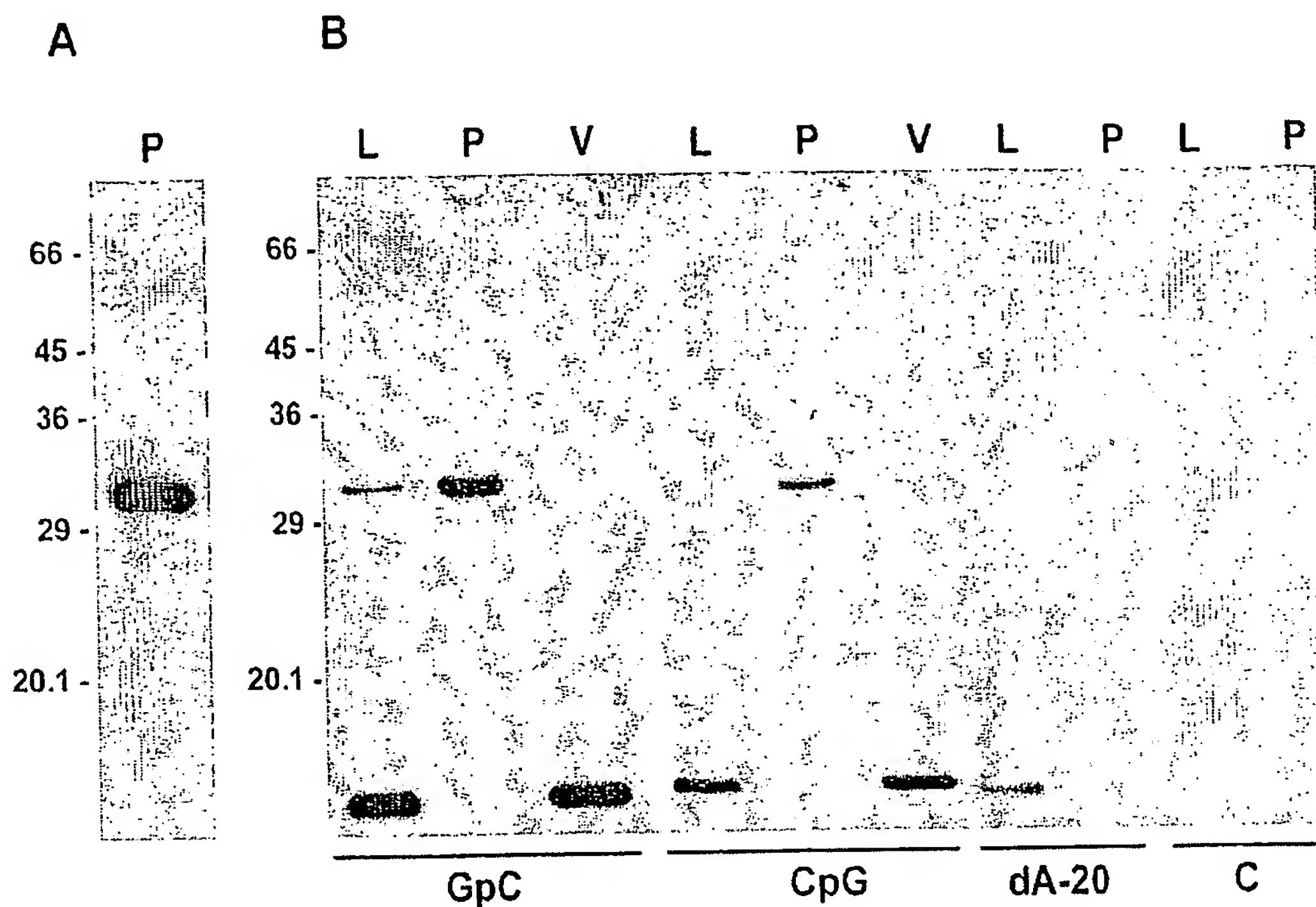
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	M S A Q A E E T A P E A A A A P V	16
51	ACCATGTCTGCTCAGGCTGAGGAAACTGCACCAAGCAGCAGCACCAGT	
	Q P S Q P A A K K K G P A S K A	32
101	ACAACCATCACACCAGCGGCCAAAAAGAAGGGACCCGCCAGTAAAGCAA	
	K P A S A E K K N K K K K G K G P	49
151	AGCCTGCCTCTGCAGAAAAAAAGAACAAAAAGAAGAAAGGGAAAGGGCCC	
	G K Y S Q L V I N A I Q T L G E R	66
201	GGAAAGTACAGCCAGCTGGTGTCAATGCTATCCAAACGCTGGGAGAGAG	
	N G S S L F K I Y N E A K K V N	82
251	AAACGGCTCGTCTCTTTAAGATCTACAACGAGGCCAGAACAGTGAAC	
	W F D Q Q H G R V Y L R Y S I R A	99
301	GGTTTGACCAGCAGCACGGCGCGTGTACCTCCGCTACTCCATCCGCGCG	
	L L Q N D T L V Q V K G L G A N G	116
351	CTGCTGCAGAACGACACGCTCGTCAGGTGAAGGGCTGGGCGCCAACGG	
	S F K L N K K K F I P R T K K S	132
401	CTCCTTCAAGCTCAACAAAAAGAAGTTCATCCCCAGAACCAAGAAGAGCT	
	S V K P R K T A K P T K K P A K K	149
451	CTGTAAAGCCGAGAAAGACTGCGAACCGACCAAAAGCCAGCCAAAAAA	
	A A K K K K R V S G V K K A T P P	166
501	GCAGCGAAGAAGAAGAAAAGGGTCAGCGCGTGAAGAAGGCGACTCCCC	
	P E K T S K P K K A D K S P A V	182
551	CCCAGAGAAAACCTCCAAACCAAGAAAGCGGATAAAAGTCCAGCCGTCT	
	S A K K A S K P K K A K Q T K K T	199
601	CTGCCAAGAAGGCGAGCAAGCCAAGAAAGCTAACAGACAAAAAAAGACT	
	A K K T *	203
651	GCTAAGAAGACTTAAACGTTATATTCTGCATGCTTGTGCATTAAGCA	
701	TTGCACTGCAGGTAAACTGCACGCTTCTGATCGCAGTTCAATTAGG	
751	ATATGCACAGTGTAAACCAAGTGTGCAAGTCACTCTGGTCTCAATGTT	
801	TACTGATGTAACCACATGTAAATAACTGTACAAAGAAGGAAACAATCACT	
851	TTTGTAAACGTCTGCTTGTATTATTCTTTCTACTAGTTAGCTAAAT	
901	AACTGCTTATGGCTTCTTTAA <u>AT</u> <u>AA</u> ATGATAAA <u>AG</u> <u>AAAAA</u> <u>AAAAA</u>	
951	<u>AAAAAA</u>	

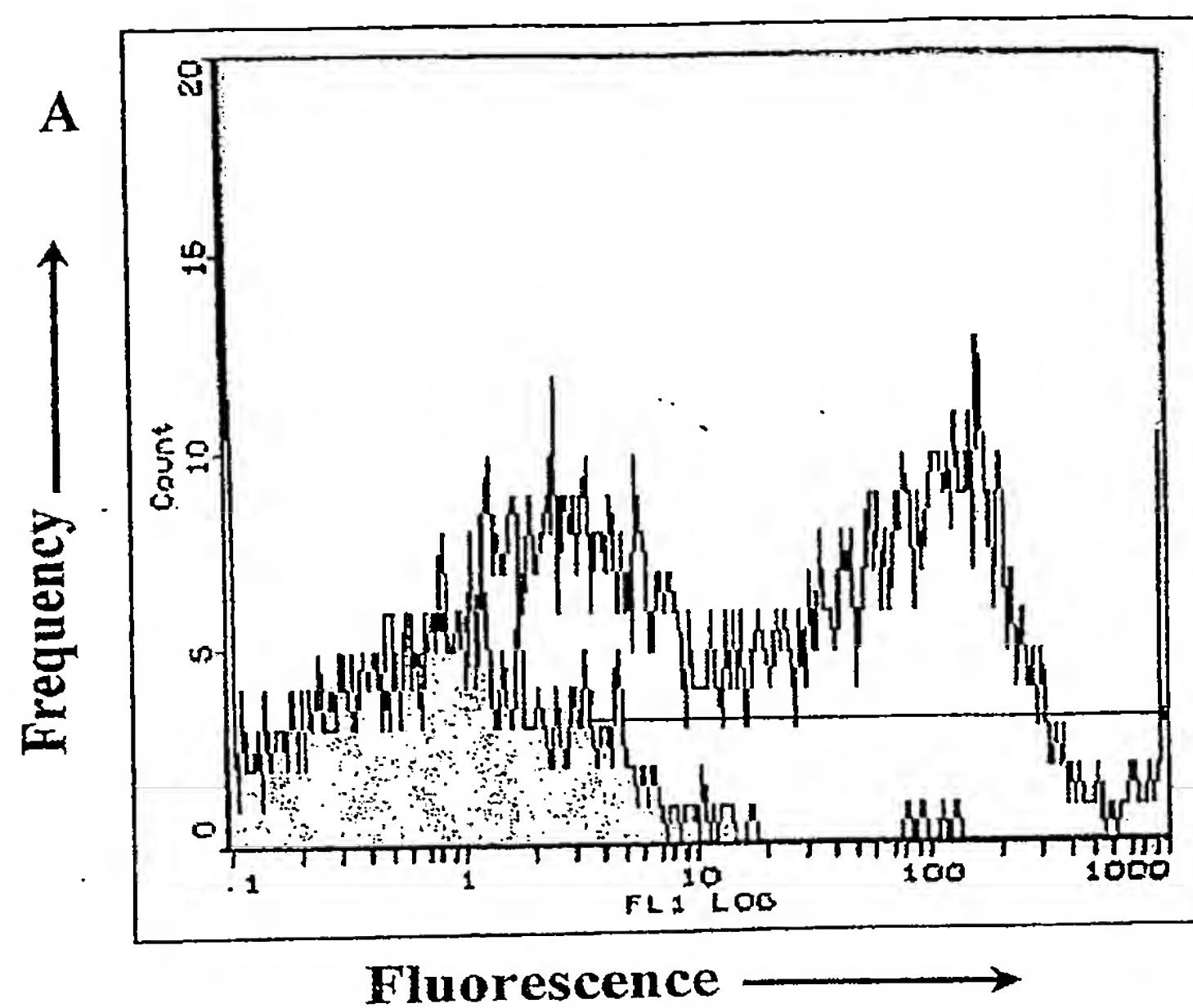
Figure 11

Catfish NCAMP-1	MSAQAEETAPEAAAPVQPSQP-----	-AAKKKGPASKAKPASAEEKRNKKKKGGKGGPKYSCTVINAQTTLGERNG	68
Danio H1X-like-AAH47192	-MPAVVEESAPAPAP-----	-AEKKDKPAAVASSPAK-----KKKKSKGPCKSKLNTDAIRTLGERNG	59
Xenopus H1X-AAH41758	-MALELEENLHSTEEEDEEEEEEDEEMRSSTRNKGAAASSSGNKKKK-----	-KKNCPGRYSCLVVDTIRKLGERNG	73
Mus H1X XP_144949	-MSVLEELALPPTSDG-----	-RKKNQPGKYSCLAVETIRKLGERNG	63
human H1X-BAA11018	-MSVLEELALPVTAAEG-----	-MAKKVTKAGGSAAALSPSKKRNSSKKKNOPGKYSQLYVETIRRLGERNG	64
[]			
Catfish NCAMP-1	SSLEKIYNEAKKVNWFDQOHGRVYLRYSTIRALLONDTLVQVKG-----	GANGSFKLINKKKFIPRTKSSVKPRKTAKPTKKPAK	148
Danio H1X-like-AAH47192	SSLEKIYNEAKKVSWFDQKNGRMYLRASTRAYVNDTLVQVKG-----	GANGSFKLINKKKLEKKPKK-AASKKATKKTEKPTSK	138
Xenopus H1X-AAH41758	SSLAKIYSEAKKVSWFDQNGRTIYKYSIKALVONDTLVQVKG-----	GANGSFRLINKKKLEGLPYDKKPPAKPSSSSSNRK	153
Mus H1X XP_144949	SSLARIYSEAKVWAFDQNGRTIYKYSIRALVONDTLVQVKG-----	GANGSEKLNRKKKLEGGAAERR-GASAASSSPAKR--	140
human H1X-BAA11018	SSLAKIYTEAKVWPFDQNGRTIYKYSIKALVONDTLVQVKG-----	GANGSEKLNRKKKLEGGERRGAPAAATAPATAHKA	144

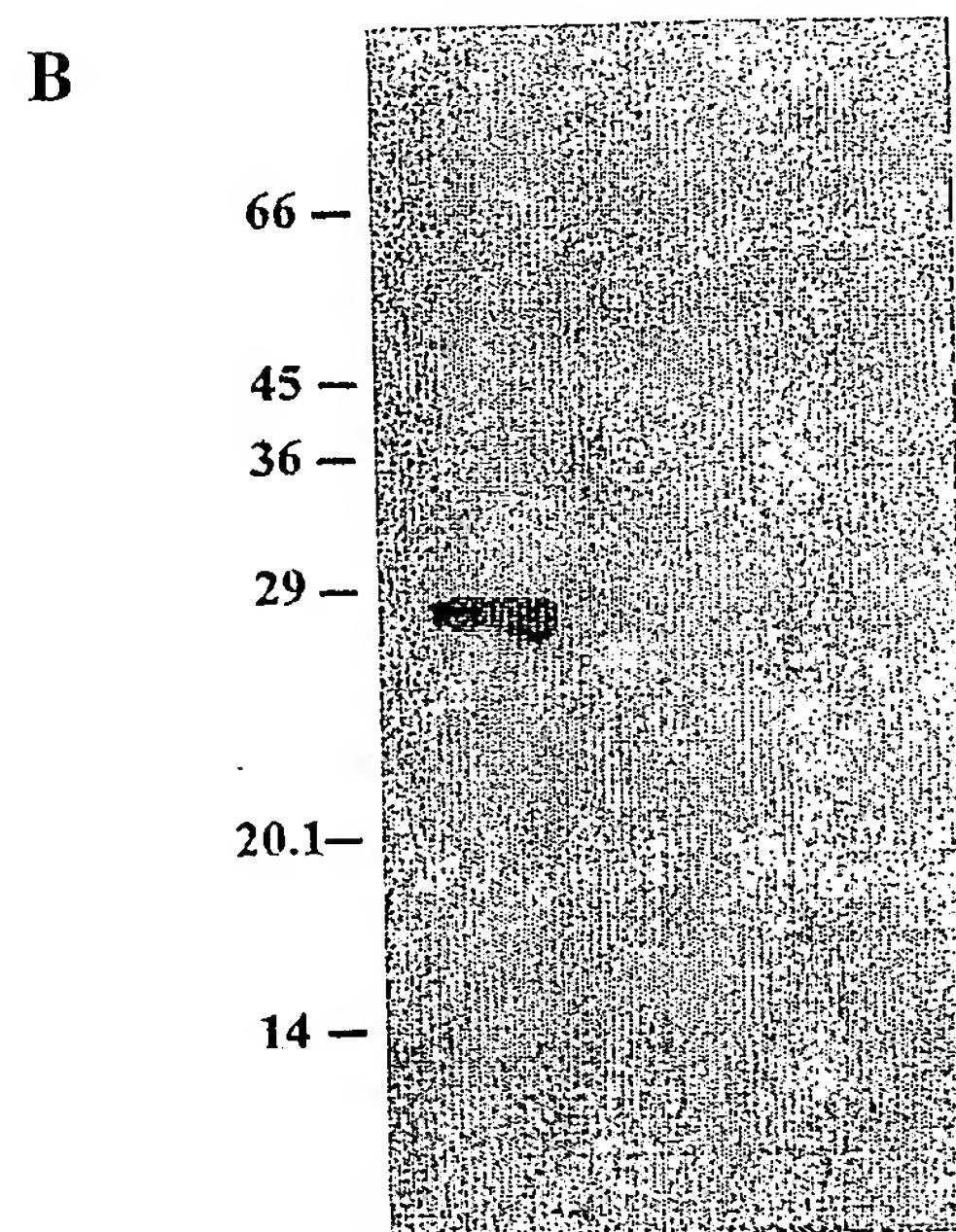
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Figure 12

Figures 13A - 13B**BEST AVAILABLE COPY**

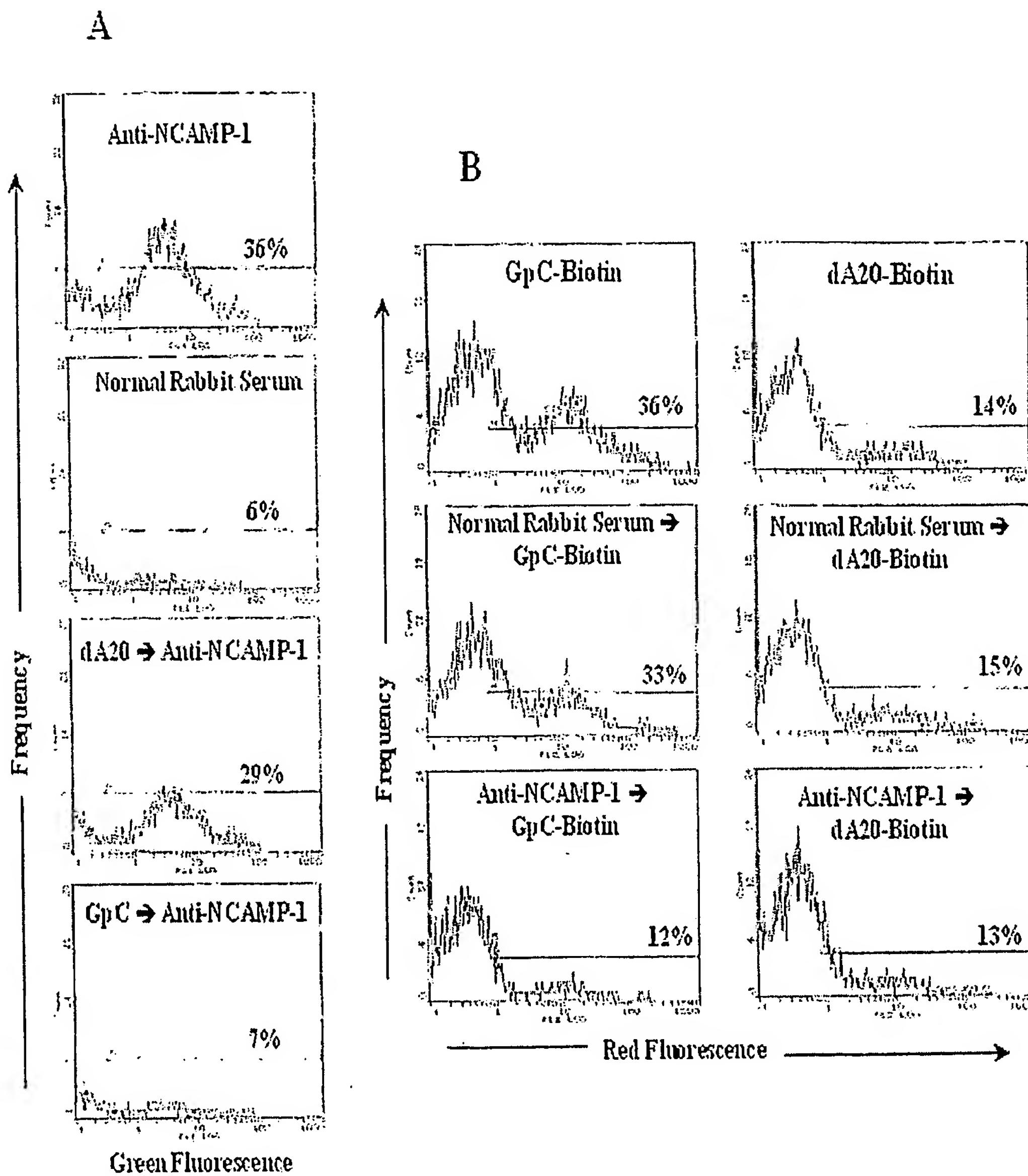
Figures 14A - 14B

1 2 3



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Figures 15A - 15B



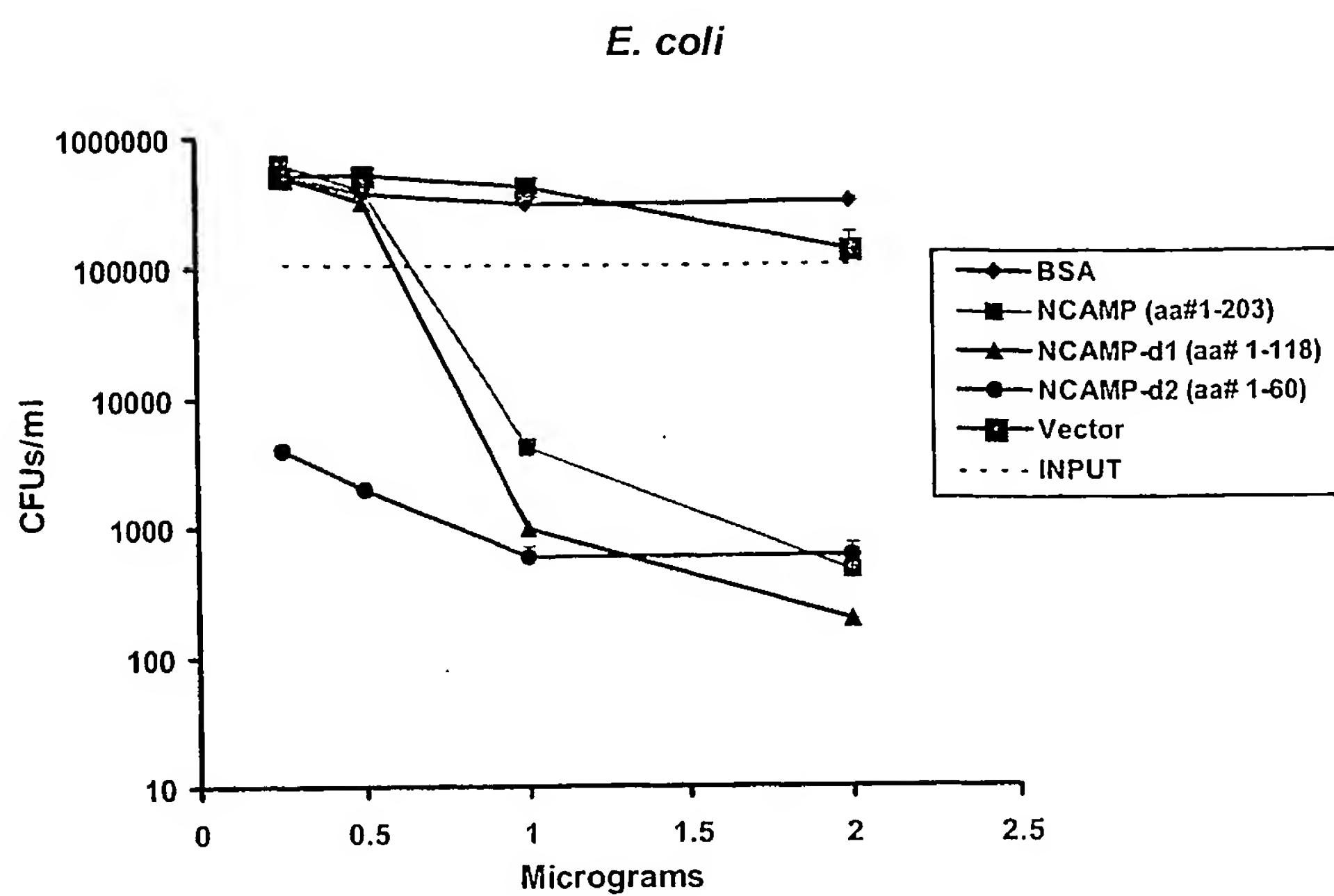
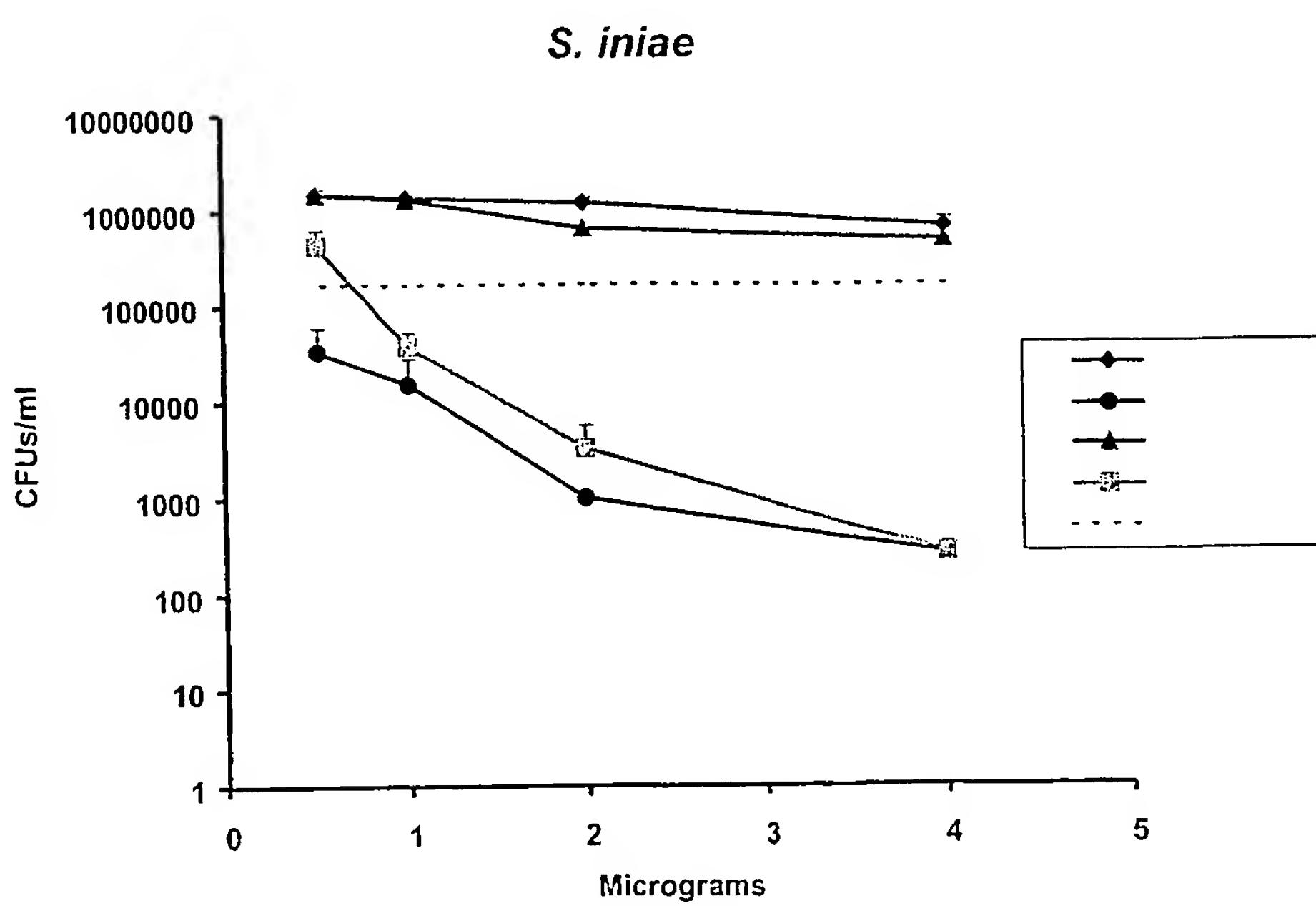
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FIGURE 16

NCAMP-1	PEAAAPVQPSQPAAKKKGPASKAKPASAEKKNKKAKGKPG
H1-Mus	-----SETAPAEKPAKAE-----
H1-Human	---KLNKKAAASGEAKPKAKAKSPKKAKA---
H1-Trout	-KAVAAKKSPKKAKKPAT--

C-Terminal residues :

NCAMP-1	
-TAKPTKKPAKKAACKKKRVSGVKKATPPPEKTSKPKKADKSPAVSAKKASKPKKAKQT	
H2A CF	--KGRGKQGGKVR AKAKT RSS--
H2B Trout	-----PDPAKTAPKKGSKKAVTKXA--
H2B Bass1	-----PEPAKSAPKKGSKKAVT-
H2B Bass2	-----PDPAPKTAPKKGSKKAVTKTAG
H1-Trout	-----AEVAPAPAAAAPAKAPKKKA
H1-Trout	-----AEVAPAPAAAAPAKAPKKAAAKPKK-----

Figures 17A - 17B**A****B****BEST AVAILABLE COPY**